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(54) Title: A PROTEIN FAMILY RELATED TO IMMEDIATE-EARLY PROTEIN EXPRESSED BY HUMAN ENDOTHELIAL CELLS DURING DIFFERENTIATION		
(57) Abstract <p>This invention provides a novel family of tissue specific genes and proteins that are related to a G-protein-coupled receptor gene and the receptor protein. The gene is an intermediate early gene that is expressed in differentiating endothelial cells. In particular, this invention provides a gene, <i>edg-1</i>, that is an immediate-early gene that encodes a G-protein-coupled receptor in endothelial cells. This invention also provides the G-protein-coupled receptor protein that is encoded by <i>edg-1</i>.</p>		

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A PROTEIN FAMILY RELATED TO IMMEDIATE-EARLY PROTEIN EXPRESSED
BY HUMAN ENDOTHELIAL CELLS DURING DIFFERENTIATION

BACKGROUND OF INVENTION

The endothelium is composed of a monolayer of quiescent cells, endothelial cells. Endothelial cells, which form the inner lining of blood vessels participate in a multiplicity of physiological functions, including the formation of a selective barrier for the translocation of blood constituents and macromolecules to underlying tissues and the maintenance of a non-thrombogenic interface between blood and tissue. Endothelial cells are also an important component in the development of new capillaries and blood vessels. Blood vessel development, which is called angiogenesis, occurs during developmental periods, such as during development of the vascular system, and as part of the pathophysiology of a variety of disease states, such as psoriasis, arthritis, chronic inflammatory conditions, diabetic retinopathy, and tumor development.

Angiogenesis, which involves the organized migration, proliferation, and differentiation of the endothelial cells, is initiated by the endothelial cell in response to angiogenic stimuli and can be separated into three distinct events: cell migration, cell proliferation and cell differentiation, whereby the cells organize into a tubular structure.

These events are mediated in vitro, and most likely in vivo, by mitogenic polypeptides. The migration of endothelial cells is induced by factors, including the heparin binding

1 growth factors and angiotropin. Proliferation is induced by
2 the heparin binding growth factors (hereinafter HBGFs) and
3 differentiation and cellular organization is induced by
4 polypeptides, including interleukin-1 (hereinafter IL-1),
5 tumor necrosis factor (hereinafter TNF), gamma-interferon,
6 transforming growth factor alpha and beta (hereinafter TGF- α
7 and TGF- β , respectively) and phorbol myristic acetate
8 (hereinafter PMA).

9 The extracellular matrix (hereinafter ECM), which
10 contains numerous components, also modulates endothelial cell
11 differentiation. If endothelial cells are cultured in vitro
12 on collagen gels in the presence of PMA organized networks of
13 tubular structures form, and, if the cells are cultured in ECM
14 conditioned medium the formation of tubular structures is
15 accelerated.

16 The importance of the ECM components for mediation of
17 endothelial cell differentiation is evidenced by the
18 observations that antibodies that have been prepared against
19 fibronectin and laminin inhibit formation of the
20 differentiated phenotype, while proteolytic modification of
21 fibronectin by plasmin leads to rapid modification of the
22 endothelial cell phenotypic changes that are observed in
23 vitro. In addition, competitive inhibitors of the laminin
24 and fibronectin receptor binding domains also inhibit the
25 ability of endothelial cells to complete the non-terminal
26 differentiation program.

27 As discussed above, the polypeptide cytokines and PMA
28 inhibit the HBGF-1-induced proliferation of endothelial cells
29 and induce differentiation thereof. These factors induce a
30 reversible phenotypic transition from a non-polar cobblestone
31 monolayer into a polar elongated, fibroblast-like phenotype.
32 The inhibition of HBGF-1-induced proliferation is mediated,
33 at least in part, via down regulation of the HBGF-1 receptor.

1 It is also known that PMA activates protein kinase C,
2 which a family of phospholipid- and calcium-activated protein
3 kinases. This activation results in the transcription of an
4 array of proto-oncogene transcription factors, including c-
5 fos, c-myc and c-jun, proteases, protease inhibitors,
6 including collagenase type I and plasminogen activator
7 inhibitor, and adhesion molecules, including intercellular
8 adhesion molecule I. Protein kinase C activation antagonizes
9 growth factor activity by the rapid phosphorylation of the
10 epidermal growth factor receptor. Phosphorylation decreases
11 tyrosine kinase activity.

12 Upon induction of differentiation of endothelial cells
13 in vitro by a cytokine or PMA, a set of immediate-early genes
14 are rapidly induced via a pathway that does not require
15 protein synthesis. Included among these immediate-early genes
16 are transcriptional factors, cytokines, cytoskeletal proteins,
17 nuclear hormone receptors and extracellular matrix receptors.

18 Cell surface receptors bind circulating signal
19 polypeptides, such as growth factors and hormones, as the
20 initiating step in the induction of numerous intracellular
21 effector functions. Receptors are classified on the basis of
22 the particular type of pathway that is induced. Included
23 among these classes of receptors are those that bind growth
24 factors and have intrinsic tyrosine kinase activity, such as
25 the HBGF receptors and those that couple to effector proteins
26 through guanine nucleotide binding regulatory proteins,
27 hereinafter referred to as G-protein coupled receptors and G-
28 proteins, respectively. The G-protein transmembrane signaling
29 pathways consist of three proteins: receptors, G proteins and
30 effectors.

31 G proteins, which are the intermediaries in transmembrane
32 signaling pathways, are heterodimers and consist of α , β and
33 gamma subunits. Among the members of a family of G proteins

1 the α subunits differ. Functions of G proteins are regulated
2 by the cyclic association of GTP with the α subunit followed
3 by hydrolysis of GTP to GDP and dissociation of GDP.

4 G-protein coupled receptors are a diverse class of
5 receptors that mediate signal transduction by binding to G-
6 proteins. Signal transduction is initiated via ligand binding
7 to the cell membrane receptor, which stimulates binding of the
8 receptor to the G-protein. The receptor-G-protein interaction
9 releases GDP, which is specifically bound to the G-protein,
10 and permits the binding of GTP, which activates the G-protein.
11 Activated G-protein dissociates from the receptor and
12 activates the effector protein, which regulates the
13 intracellular levels of specific second messengers. Examples
14 of such effector proteins include adenylyl cyclase, guanylyl
15 cyclase, phospholipase C, and others.

16 G-protein-coupled receptors, which are glycoproteins, are
17 known to share certain structural similarities and homologies
18 (see, e.g., Gilman, A.G., Ann. Rev. Biochem. 56: 615-649
19 (1987), Strader, C.D. et al. The FASEB Journal 3: 1825-1832
20 (1989), Kobilka, B.K., et al. Nature 329: 75-79 (1985) and
21 Young et al. Cell 45: 711-719 (1986)). Among the G-protein-
22 coupled receptors that have been identified and cloned are the
23 substance K receptor, the angiotensin receptor, the α - and β -
24 adrenergic receptors and the serotonin receptors. G-protein-
25 coupled receptors share a conserved structural motif. The
26 general and common structural features of the G-protein-
27 coupled receptors are the existence of seven hydrophobic
28 stretches of about 20-25 amino acids each surrounded by eight
29 hydrophilic regions of variable length. It has been
30 postulated that each of the seven hydrophobic regions forms
31 a transmembrane α helix and the intervening hydrophilic
32 regions form alternately intracellularly and extracellularly

-5-

1 exposed loops. The third cytosolic loop between transmembrane
2 domains five and six is the intracellular domain responsible
3 for the interaction with G-protein.

4 G-protein-coupled receptors are known to be inducible.
5 This inducibility was originally described in lower
6 eukaryotes. For example, the cAMP receptor of the cellular
7 slime mold, Dictyostelium, is induced during differentiation
8 (Klein et al., Science 241: 1467-1472 (1988). During the
9 Dictyostelium discoideum differentiation pathway, cAMP,
10 induces high level expression of its G-protein-coupled
11 receptor. This receptor transduces the signal to induce the
12 expression of the other genes involved in chemotaxis, which
13 permits multicellular aggregates to align, organize and form
14 stalks (see, Firtel, R.A., et al. Cell 58: 235-239 (1989) and
15 Devreotes, P., Science 245: 1054-1058 (1989)). H u m a n
16 endothelial cells utilize a series of morphological correlates
17 during its differentiation pathway, discussed supra., in which
18 individual cells migrate, align and organize to form
19 multicellular capillary-like structures.

20 SUMMARY OF THE INVENTION

21 It is one object of this invention to provide a novel G-
22 protein-coupled receptor that is the product of an immediate
23 early gene that is expressed in endothelial cells during the
24 early stage of differentiation.

25 It is another object of this invention to provide a
26 family of proteins that are expressed in a tissue-specific
27 manner and that are related to the novel G-protein-coupled
28 receptor that is the product of an immediate early gene that
29 is expressed in endothelial cells during the early stage of
30 differentiation.

1 It is another object of this invention to provide DNA
2 molecules that encode each member of the family of proteins
3 that are expressed in a tissue-specific manner and that are
4 related to the novel G-protein-coupled receptor that is the
5 product of an immediate early gene that is expressed in
6 endothelial cells during the early stage of differentiation.

7 It is another object of this invention to provide DNA
8 molecules that encode the novel G-protein-coupled receptor
9 that is the product of an immediate early gene that is
10 expressed in endothelial cells during the early stage of
11 differentiation.

12 In accordance with this invention there is provided a DNA
13 molecule that encodes edg-1 gene product, which is the product
14 of an immediate-early gene that is expressed in the early
15 stage of differentiation of endothelial cells in response to
16 PMA or IL-1.

17 This invention provides a gene and protein, which is the
18 first immediate-early gene that encodes a G-protein-coupled
19 receptor.

20 Unless defined otherwise, all technical and scientific
21 terms used herein have the same meaning as is commonly
22 understood by one of ordinary skill in the art to which this
23 invention belongs. Although methods and materials similar or
24 equivalent to those described herein can be used in the
25 practice of testing of the present invention, the preferred
26 methods and materials are now described. All publications
27 mentioned hereunder are incorporated by reference.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. The identification of *edg-1*, an Immediate early gene induced by PMA in HUVEC (human umbilical vein endothelial cells).

Confluent cultures of HUVEC were treated with 20 ng/ml of PMA for the indicated times. The cells were then lysed, RNA purified, and total RNA (10 µg) analyzed by Northern blot analysis. The cDNA probes that were used were *edg-1* (A) and glyceraldehyde-3-phosphate (GAPDH) (B) cDNA.

Figure 2. Confluent cultures of HUVEC were treated with the indicated reagents for 4 hour and the RNA was isolated. Total RNA (10 µg) was fractionated by 1% agarose-formaldehyde gel electrophoresis, blotted onto a zeta-probe membrane and hybridized with [³²P]-labeled *edg-1* (A) or a GAPDH (B) cDNA probes. The following reagents were used: PMA (20 ng/ml), chx (5 µg/ml), Actinomycin D (Act D) (2 µg/ml). Each reagent was used either alone or in combination.

Figure 3. Confluent cultures of HUVEC were pre-treated with 20 ng/ml PMA for 4 hour. Either Act D (2 µg/) alone or with chx (5 µg/ml) was added to the cultures, at a time designated 0. At the indicated time points, cultures were harvested and Northern blot analysis was performed on total RNA as described above using the *edg-1* (A) and GAPDH (B) cDNA probes.

Figure 4. HUVEC were either untreated or treated with 20 ng/ml PMA for 2 hour after which nuclei were prepared. Run-off transcripts were obtained by labelling 10⁷ nuclei in vitro with [³²P]-UTP. RNA was purified and hybridized to immobilized plasmid DNA encoding *edg-1* (10 µg/slot), human fibronectin (fn) (2 µg/slot) and pBluescript (pBS) (10 µg/slot).

1 Figure 5. Nucleotide and Deduced Amino Acid Sequence of
2 Human edg-1.

3 The nucleotide (1-2774) and deduced amino acid sequence
4 (1-380) is shown for human edg-1 cDNA. The deduced
5 transmembrane domains are underline and potential N-linked
6 glycosylation sites are shown with ann asterisk. Possible
7 serine and threonine phosphorylation sites are shown with
8 closed circles. The basic amino acid-rich intracellular
9 domain, which is located between transmembrane domains five
10 and six is highlighted with open circles. The Kozak consensus
11 translation initiation sequence (5') and polyadenylation sites
12 (3') are shown with double lines underneath their respective
13 sequences. The Genbank accession number for this nucleotide
14 sequence is M31210.

15 Figure 6. The amino acid sequence of the putative edg-
16 1 translation product was aligned with Substance K receptor
17 (SKR), Substance P receptor (SPR), β_2 -adrenergic receptor
18 (B2AR), Serotonin receptor 1c (5HTC), α_2 -adrenergic receptor
19 (A2A), Serotonin receptor 1a (5HT1a), Rhodopsin (OSPD) and
20 angiotensin receptor (MAS). Highly homologous regions are
21 boxed and indicated on the linear schematic.

22 Figure 7. A structural model for the putative edg-1
23 translation product is shown. This model is analogous to other
24 G-protein-coupled receptors. The potential N-linked
25 glycosylation sites are indicated with an inverted "Y".
26 Potential phosphorylation sites at serine and threonine
27 residues are shown with dark circles. The third cytosolic
28 intracellular domain, which is between transmembrane domains
29 5 and 6 contains a highly basic region (11/35 residues) is
30 also indicat d.

-9-

Figure 8. Hydrophobicity Profile of edg-1 Translation Product. The deduced amino acid sequence of edg-1 was analyzed for hydrophobic regions and the amino acid sequence (residues) plotted against the hydrophobicity index. The putative transmembrane (TM) domains are indicated.

Figure 9. Expression of edg-1 transcript in human cells. Total RNA (5 μ g) from human saphenous vein smooth muscle cells (S), foreskin fibroblasts (F), HeLa cells (H), epidermoid carcinoma (A431) cells (A), melanocytes (M), brain tissue (B) and endothelial cells (E) were reverse transcribed into cDNA and amplified with edg-1 specific oligonucleotide primers that span the carboxy-terminal tail domain (A) and the third cytosolic loop (B). Amplified DNA was separated by agarose gel electrophoresis and visualized by ethidium bromide staining. Molecular weight markers (indicated by arrows) are from top to bottom: 1.6 Kb, 1.0 Kb, 0.5 Kb, 0.4 Kb, 0.3 Kb, 0.2 Kb and 0.15 Kb.

It can be seen in (A) that transcript of the expected size, about 600 bp,, which was amplified using oligonucleotide primers specific for the C-terminal domain, was present in RNA from all the cultured cell lines and human brain. In contrast, when the transcript was amplified using an a pair oligonucleotides that span the third intracellular loop, cell or tissue specific bands were observed.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

In the invention described herein a novel gene, edg, and the protein encoded thereby has been identified. In addition, this invention provides a family of proteins that are structurally and functionally related to this protein as well as DNA molecules, but that are tissue or cell type specific are provided.

-10-

1 As used herein, the edg-G-protein-coupled receptor family
2 is a family of related proteins that share substantial
3 homology and structure and that contain common constant
4 regions or domains but differ in at least one variable region
5 or domain that includes the third cytosolic loop. See, e.g.,
6 Figures 6, 7, and 9. The particular variable region and,
7 thus, each family member, is expressed in a tissue-specific
8 manner.

9 As used herein, expression of a transcript in a tissue-
10 specific manner includes expression of transcripts that are
11 expressed in only certain tissues or cell types. Such tissue-
12 specific expression can be effected through a variety of
13 mechanisms, including the expression of different genes in
14 each tissue or cell type, through alternative splicing of the
15 same gene in each tissue or cell type, or through
16 recombination of germ line DNA in during development or
17 differentiation of each cell type.

18 As used herein, the edg-1-G-coupled protein receptor
19 transcript is the intermediate early transcript that is
20 expressed in the early stage of differentiation in endothelial
21 cells that can be induced or stimulated with PMA and
22 interleukin-1 (IL-1) but not with TGF- β , HBGF-1, or α -
23 thrombin. The edg-1 G-coupled protein receptor transcript
24 encodes the edg-1 G-coupled protein receptor.

25 As used herein, the edg-1-G-coupled protein receptor
26 transcript family is a family of transcripts that are
27 expressed in a tissue-specific manner and encode members of
28 the family of related proteins that share substantial homology
29 and structure and that contain common constant regions or
30 domains but differ in at least on variable regi n that
31 includes the third cytosolic loop.

-11-

1 As used herein, DNA encoding a protein includes any DNA
2 molecule that encodes a protein that has substantially the
3 same amino acid sequence. Each of such proteins may, however,
4 differ at sites that are not essential to protein function and
5 includes proteins isolated from different individuals in the
6 same species, proteins isolated from different species that
7 share substantially the same biological activities, and
8 proteins isolated from different cultured cell lines.

9 As used herein, the *edg-1* transcript refers to the 2.8
10 Kb (about 3 Kb) transcript that encodes the receptor protein.
11 This term is herein used interchangeably with the *edg*
12 transcript, *edg* mRNA. The *edg-1* transcript also refers to this
13 transcript, but also refers to the 1-Kb clone that was
14 isolated from the differential screen, which contained a poly
15 A tract at 3' end, a unique nucleotide sequence and hybridized
16 to the about 3.0 Kb PMA inducible mRNA species, the *edg-1*
17 transcript.

18 Because PMA inhibits endothelial cell proliferation and
19 induces differentiation, the identification and isolation of
20 immediate-early genes yields insight into the molecular
21 mechanisms involved in the regulation of endothelial cell
22 differentiation.

23 Immediate-early genes that are expressed in endothelial
24 cells may be isolated from any source of endothelial RNA. In
25 one embodiment of this invention, human umbilical vein
26 endothelial cells (hereinafter HUVEC) are used. The HUVEC are
27 either untreated and treated with PMA, IL-2 or any other
28 signal that induces these genes.

-12-

1 The desired immediate-early genes can be identified by
2 any means in which the transcripts comparing the transcripts
3 in cells that are stimulated with PMA, IL-2 or other inducer
4 with the transcripts that are present in untreated cells.
5 Those that are present only in the treated cells are, thus,
6 immediate-early genes. In addition, any member of the G-
7 protein-coupled receptor family of this invention can be
8 identified by screening an appropriate library with an
9 appropriate probe derived from the edg-1 clone. For example,
10 an appropriate probe would be one derived from the 3' end of
11 the clone. Any methods known to those of skill in the art to
12 accomplish this may be used.

13 In endothelial cells the immediate-early gene of this
14 invention is the edg-1 encoding gene. It is induced by IL-1,
15 LPS or PMA, but not by HBGF-1, TGF- β , or α -thrombin. The edg-
16 1 clone provided herein encodes a protein that shares many
17 structural and sequence similarities with known G-protein-
18 coupled receptors, including the β -adrenergic, substance K,
19 substance P, rhodopsin, serotonin (5-HT), tachykinin receptors
20 and the cAMP receptor of Dictyostelium.

21 The N-linked glycosylation site at Asn₃₀ is also found in
22 the Substance K and angiotensin receptors. The two N-linked
23 glycosylation sites are found within the amino-terminal domain
24 of all G-protein-coupled receptors. The region in proximity
25 to the second and third hydrophobic domains is highly
26 conserved among all such receptors, including that encoded by
27 edg-1. In the β_2 -adrenergic receptor Asp₁₃₀ is known to be
28 absolutely necessary for G-protein; in the edg-1-encoded
29 protein the Asp/Glu-Arg is conserved.

30 Although the overall sequence similarity between the
31 edg-1 G-protein-coupled receptor of this invention and other
32 such receptor is quite divergent, there is a significant
33 degree of sequence similarity within the carboxy-terminal

-13-

1 half, particularly within transmembrane domain seven. It is
2 most similar to those receptors that recognize peptides as
3 receptor ligands.

4 The intracellular hydrophilic loop regions contain four
5 potential phosphorylation sites at residues Thr₇₂, Ser₂₃₁, Thr₂₃₅
6 and at Ser₃₅₁. This feature is common to many G-protein-
7 coupled receptors. Phosphorylation at the Ser and Thr
8 residues within the intracellular domains has been implicated
9 in the phenomenon of receptor desensitization.

10 The hydrophilic region between transmembrane domains five
11 and six is the region that is absolutely necessary for G-
12 protein coupling and it is highly divergent among members of
13 the G-protein-coupled receptor proteins. In the G-protein-
14 coupled receptor that is encoded by *edg-1*, this region is
15 highly basic. The family of *edg-1* related tissue-specific
16 proteins provided in this invention differ in this region and,
17 thus, most likely differ in their respective binding or
18 coupling interactions with the G-protein or protein ligands.

19 The ligand that binds to each of the members of the
20 family of G-protein-coupled receptor proteins of this
21 invention can be identified by methods that are known to those
22 of skill in the art. For example, *xenopus* oocytes can be
23 transfected with DNA that encodes the particular protein. The
24 protein will be expressed on the cell surface of the oocytes.
25 Since these oocytes are sensitive to calcium exchange across
26 the cell membrane, binding of the appropriate ligand causes
27 calcium exchange across membrane. Labeled calcium can be used
28 and the ligand that causes labeled calcium exchange can be
29 identified. Among the candidates for the ligand that binds
30 to the *edg-1*-G-protein coupled receptor are ATP, AMP,
31 adenosine, leukotrienes, prostenoids, histamine, bombasin,
32 thrombin, azopressin, bradykinin, endothelin, serotensin,
33 substance P and neuropeptide.

-14-

1 The following examples are included for illustrative
2 purposes only and are not intended to limit the scope of the
3 invention.

4 EXAMPLE 1

5 Materials and Cell Culture

6 Recombinant human interleukin α (IL-1 α), which was the
7 gift of Dr. Peter Lomedico, Hoffman La Roche, Nutley, NJ.
8 Recombinant human HBGF-1 α was obtained from Anthony Jackson,
9 American Red Cross, Rockville, MD. Porcine TGF- β was purchased
10 from R & D Systems.

11 Primary cultures of human umbilical vein endothelial
12 cells (HUVEC) were obtained from Dr. Michael Gimbrone, Harvard
13 Medical School, Boston, MA, and were grown on fibronectin-
14 coated plates in Medium 199 supplemented with 10% (v/v) fetal
15 bovine serum, 1x antibiotic and antimycotic mixture (GIBCO,
16 Grand Island, NY), 150 μ g/ml crude endothelial cell growth
17 factor (Maciag et al., 1981) and 5 U/ml heparin (Sigma) as
18 described in Maciag et al. ((1981) J. Biol. Chem. 91, 420-
19 426). Cells were subcultured at a 1:5 split ratio and
20 cultures between passages of 4 and 12 were used. At
21 confluence, cells were maintained in medium without the growth
22 factor and heparin for two days to achieve quiescence.

23 RNA Preparation and cDNA Library Construction

24 Total RNA was obtained from cells that either untreated
25 or treated with 20 ng/ml PMA (Sigma) and 5 μ g/ml of
26 cycloheximide (hereinafter chx) (Sigma) for 4 hours. The
27 cells were rinsed with phosphate-buffered saline, lysed in 4M
28 guanidinium isothiocyanate and total RNA purified as described
29 in Winkles, J., et al. ((1987) Proc. Natl. Acad. Sci. USA 84,

-15-

1 7124-7128). Poly A⁺ RNA (10 µg) from HUVEC exposed to PMA
2 and chx was converted to double-stranded cDNA and cloned into
3 the Eco R1 site of lambda gt10, using the cDNA synthesis kit
4 from Bethesda Research Labs (Gaithersburg, MD) and the cDNA
5 cloning kit from Amersham (Chicago, IL). The library contained
6 > 10⁶ independent clones, with an average insert size of
7 approximately 1 Kb.

8 Northern Blot Analysis.

9 Total RNA (10 µg) was electrophoresed on a 1% agarose
10 gel containing 2.2 M formaldehyde, capillary-blotted onto
11 Zeta-probe membrane (Biorad) and UV cross-linked (Maniatis et
12 al. (1982) In Molecular Cloning: A Laboratory Manual, Cold
13 Spring Harbor Laboratory, Cold Spring Harbor, NY). The cDNA
14 insert fragment for edg-1 (2.8 Kb) or human GAPDH (1 Kb) was
15 labeled to high specific activity (>10⁸ cpm/µg) using a random
16 primer labeling kit (BRL) and was used to hybridize filters
17 in Church-Gilbert buffer (0.5 M sodium phosphate pH 7.2,
18 containing 7% SDS and 1% bovine serum albumin, 1mM EDTA and
19 20% formamide at 65° C for 16-20 hrs. Filters were washed
20 twice for 15 min at high-stringency (0.1xSSC, 65° C).

21 Differential Screening of cDNA Library

22 The differential screen was performed by plating 2 x 10⁶
23 pfu of the library onto bacteriological plaques (15 cm
24 diameter) containing LB agar. The phage were allowed to grow
25 at 37° C until plaques were approximately 0.5 mm in diameter.
26 Phage DNA was adsorbed onto Gene-screen plus nylon filters
27 (Dupont, DE), in duplicate, denatured, neutralized, and UV
28 cross-linked.

-16-

1 The probe for differential screening was prepared by
2 reverse transcription of 1 μ g of poly A⁺ RNA from control and
3 PMA/chx-treated HUVEC. The reaction conditions were as
4 follows: 50 mM Tris HCl, pH 8.3, 75 mM KCl, 20 mM
5 dithiothreitol, 3 mM MgCl₂, 500 μ Ci [³²P]- α -dCTP, 20 μ M dCTP,
6 200 μ M each of dATP, dCTP, and dTTP, 0.5 μ g/ml of oligo dT₁₂₋₁₈
7 and 400 units of MMLV-reverse transcriptase (Bethesda
8 Research Labs, Gaithersburg, MD).

9 After incubation at 37° C for 60 minutes, RNA was
10 hydrolyzed by treatment with 100 μ l 0.6M NaOH and 20 mM EDTA
11 for 30 minutes at 65° C. The cDNA was purified on Sephadex
12 G-50 columns and ethanol-precipitated. Duplicate filters were
13 incubated with 10 cpm/ml of cDNA for 48 hours at 65° C in
14 hybridization buffer containing 2% SDS, 1 M NaCl and 10%
15 dextran sulfate. The filters were washed twice for 30 min at
16 65° C with 2xSSC containing, 1% SDS followed by two additional
17 washes for 30 min at 65° C with 0.1xSSC containing 1% SDS.

18 The filters were autoradiographed and duplicates were
19 superimposed on each other to isolate PMA/chx-induced signals.
20 Differential signals were plaque-purified by repeating the
21 screening process. Insert cDNA was prepared and used for either
22 Northern blot analysis or subcloning into plasmid vectors.

23 Of the twelve positive signals obtained from >10⁵ pfu of
24 the library three were found to be consistently positive. Two
25 of the clones had inserts had sequences identical to the
26 sequence of DNA that encodes human collagenase Type 1. The
27 third clone, herein called edg-1 (1-Kb) contained a poly A
28 tract at 3' end, a unique nucleotide sequence and hybridized
29 to a 3.0 Kb PMA inducible mRNA species.

30 This 1 kb insert was used to rescreen two additional cDNA
31 libraries-lambda gt10 and cDM8. The largest clone was 2.8
32 kb. Further investigation and analysis was conducted using
33 this clone, which is expressed at high levels (0.05%) in the
34 HUVEC.

-17-

EXAMPLE 2

The kinetics of edg RNA induction by PMA was studied by Northern blot analysis of HUVEC that were exposed to PMA for 0.5, 1, 2, and 4 hours (Figure 1 (A)).

In order to determine the characteristics of the rapid edg-1 induction, Northern blot analysis was performed with HUVEC that had been treated for 4 hours with PMA and chx, alone or in combination (Figure 2). As can be seen in Figure 2, the 3.0 KB mRNA edg transcript was induced independently by PMA and chx, but was superinduced in the presence of both.

EXAMPLE 3

Chx was shown to exert the superinduction effect by stabilizing the edg-1 transcript (Figure 3). HUVEC were stimulated for 4 hour with PMA and subsequently incubated with actinomycin D, in inhibitor of transcription both in the presence and absence of chx. As shown in Figure 3 steady-state levels of the edg-1 mRNA declined to undetectable levels two hours after the addition of actinomycin D; whereas, chx prevented this decline.

EXAMPLE 4

In order to ascertain at what level PMA induces edg-1 mRNA, edg 1 induction in the presence of actinomycin D was investigated. As shown in Figure 2, actinomycin D repressed the inductive effect of PMA, which suggests that PMA induces the transcription of the edg-1 gene.

EXAMPLE 5Nuclear Run-On Transcription.

Nuclei (10^7) were prepared from quiescent HUVEC untreated or treated with 20 ng/ml PMA for 2 hr. *In vitro* labeled, run-off transcripts were prepared by incubating the nuclei with 250 μ Ci of [α - 32 P]-UTP (.6000 Ci/mmol, Amersham), 10mM ATP, CTP, GTP, in the reaction buffer containing 20mM Tris-HCl, pH 7.9, 140mM KCl, 10mM MgCl₂ and 1mM dithiothreitol as described (Nevins, J., (1987) Meth. Enzymol. 152, 234-240).

The labeled RNA was purified (Winkles, J., supra.) and hybridized to nylon filters containing either 10 μ g of denatured plasmid *edg-1* cDNA, 2 μ g of human fibronectin or 10 μ g of pBluescript (Stratagene). The hybridization and washing conditions were identical to those described for the differential hybridization.

Nuclei were prepared from untreated HUVEC or from HUVEC treated with PMA for 2 hours. Labeled run-on transcripts were obtained and hybridized to immobilized plasmid DNA containing the *edg-1* insert and to a control plasmid containing fibronectin-encoding DNA or to a Bluescript plasmid (Figure 4). *Edg-1* transcription was significantly induced in nuclei from the PMA treated HUVEC.

EXAMPLE 6DNA Sequence Analysis.

The structure of the *edg-1* gene and gene product was elucidated by DNA sequencing of the 2.8 Kb cDNA clone.

Plasmid DNA for *edg-1* (2.8Kb) was obtained by screening a cDNA library from HUVEC constructed in the vector, cDM8, which was a gift of Brian See, Harvard Medical School) with the (1.6Kb) insert obtained from the cDNA library in lambda

1 gt10, discussed in Example 1. Double-stranded sequence
2 analysis was performed using the sequenase-2 enzyme (USBC),
3 following the manufacturer's instructions. Successive
4 primers were synthesized and used to sequence both strands of
5 the cDNA clone. The DNA sequence was analyzed by the
6 Intelligenetics Sequence Analysis program.

7 As shown in Figure 5, the complete nucleotide sequence
8 of the edg-1 cDNA clone is 2774 bp long and, at nucleotide 251
9 from the 5' end, contains a consensus translation initiation
10 sequence, which is followed by an open-reading frame (ORF)
11 that encodes 380 amino acids. The ORF is followed by a 3',
12 A/T-rich, 1.3 Kb untranslated region followed by a poly A
13 tail. A/T rich sequence motifs in 3' untranslated regions have
14 been implicated in conferring rapid RNA degradation of
15 intermediate-early mRNAs. There are two consensus
16 polyadenylation sites (AATAAA) at nucleotides 2590 and 2737,
17 respectively. The edg-1 clone also contains about 250 bp of
18 5' untranslated region.

19 The deduced amino acid sequence contains a non-
20 hydrophobic amino-terminal stretch of 46 amino acids, which
21 contain two potential N-linked glycosylation sites at residues
22 29 and 35. This stretch is followed by seven alternating
23 stretches of hydrophobic regions, each about 20 amino acid
24 residues long. There are 8 hydrophilic regions. Each of the
25 hydrophobic regions is flanked by hydrophilic regions of 7 to
26 19 amino acids, except for the region between the fifth and
27 sixth transmembrane domain, which is 35 residues long and is
28 rich in basic and dibasic residues. The last transmembrane
29 domain is followed by a long, 66 amino acid, stretch of
30 hydrophilic residues that include an abundance of serine and
31 threonine residues.

EXAMPLE 7Reverse Transcriptase-Polymerase Chain Reaction Analysis

RNA from HUVEC was purified as described in Example 1. RNA from human saphenous vein smooth muscle cells, human foreskin fibroblasts, human epidermoid carcinoma cells (A431), human cervical carcinoma cells (HeLa), human melanocytes and total brain were the generous gift of Dr. Jeffrey Winkles of the American National Red Cross.

Total RNA (5 µg) from all the cultured cells and poly A⁺RNA (1 µg) from human brain (Clontech) was converted to cDNA by treatment with 200 units of MMLV reverse transcriptase (Bethesda Research Labs, MD) in 50 mM Tris-HCl, pH, 8.0, 1 mM dithiothreitol, 15 mM NaCl, 3 mM MgCl₂, 1 unit RNasin (Promega), 0.2 µg of random hexamer primers, 0.8 mM dNTPs and incubated for 1 hour at 37° C. The reaction was terminated by heating at 95° C for 10 minutes and diluted to 1 ml with distilled water.

Enzymatic amplification was done on a 10 µl aliquot of the cDNA mix. PCR was performed in 50 mM Tris-HCl, pH, 8.0, 1.5 mM MgCl₂, 10 mM KCl, 0.2 mM dNTPs, 0.5 µg each of primers for edg-1 and 2.5 units of Taq DNA polymerase (Cetus, CA) (see, Saiki et al. (1988) Science 239, 487-491). The reaction mixture was heated at 94° C for 1 minute, annealed at 55° C for 2 minutes, and extended at 72° C for 3 minutes for 30 repetitive cycles. The primers used were as follows:

(1) 5'-TG TAC TGC AGA ATC TAC T-3' (sense) and 5'-T GCA GCC CAC ATC CAG CAG CA-3' (antisense) to amplify from nucleotide no. 909 to 1094, which spans the third cytosolic domain; and

(2) 5' AAG ACC TGT CAC ATC CTC TTC-3' (sense) and 5' ATG AAC CCT TTA GGA GCT TGA CAA-3' (antisense) to amplify from nucleotide no. 1100 to 1702, which spans the seventh transmembrane domain, the cytosolic tail and part of the 3'untranslated region.

1 When RNA from the various cultured human cell lines and
2 from human brain was reverse transcribed and the cDNAs
3 amplified using the oligonucleotides that are specific for the
4 C-terminal domain (amino acids 266 to the termination codon
5 and 309 bp of the 3' untranslated region, nucleotides 1100 to
6 1702, see, e.g., Figures 5-7 and 9) an amplified product is
7 the expected size, 600 bp., is observed (see Fig. 9 (A)) in
8 RNA from all cell types and human brain. The intensity of the
9 signal was most prominent in endothelial cells, but was
10 present to a lesser extent in smooth muscle cells,
11 fibroblasts, epidermoid cells, melanocytes, and brain tissue.

12 When the cDNAs were amplified with a pair of
13 oligonucleotides that span the third intracellular loop (amino
14 acids 220-282, nucleotides 909-1094), cell-specific bands were
15 amplified (Figure 9 (B)). In smooth muscle cells, a major
16 band at 0.7 Kb and minor bands at 0.9, 0.3, and 0.19 Kb were
17 observed. In HeLa cells a very prominent band was observed
18 at 0.3 Kb. The expected 0.19Kb amplification product was
19 observed only in endothelial cells.

20 This result indicates that cDNAs derived from mRNAs that
21 are related to, but not identical with, the *edg-1* transcript
22 are present in different cell types and tissues. Because the
23 third cytosolic loop has been identified in other G-protein-
24 coupled receptors as the region that binds to the G-protein,
25 the tissue specific transcripts differ in the region that
26 encodes the portion of the receptor that couples with the G-
27 protein and thereby modulates the cellular response of the
28 particular cell type to the specific signal.

29 Since modifications will be apparent to those of skill
30 in the art, it is intended that this invention be limited only
31 by the scope of the appended claims.

1 We claim:

2 1. A purified DNA molecule that encodes a protein having
3 the sequence of amino acids set forth in Figure 5.

4 2. The purified DNA molecule having the sequence of
5 nucleotide bases set forth in Figure 5.

6 3. A purified protein that has substantially the same
7 amino acid sequence as the sequence of amino acids set forth
8 in Figure 5.

9 4. A purified DNA molecule that encodes the protein of
10 claim 3.

11 5. A protein that includes regions that are
12 substantially homologous with all or a portion of the protein
13 of Figure 5, wherein said portion consists of the amino acids
14 that comprise the transmembrane domains of the protein of
15 Figure 5.

16 6. A protein selected from the group consisting of the
17 edg-1-G-coupled-protein receptor family of proteins.

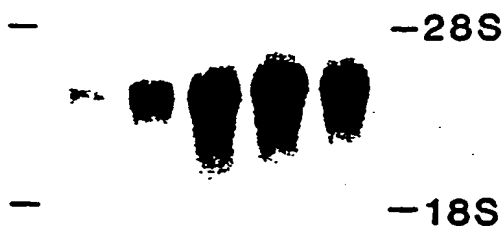
18 7. The protein of claim 6, that is expressed in a cell
19 or tissue selected from the group consisting of smooth muscle
20 cells, fibroblasts, cultured immortal human cell lines,
21 epidermoid carcinoma cells, melanocytes, brain tissue and
22 differentiating endothelial cells.

23 8. An isolated DNA molecule that encodes the protein of
24 claim 7.

1/13

FIG. 1

(A) 0 .5 1 2 4 hrs.



(B)

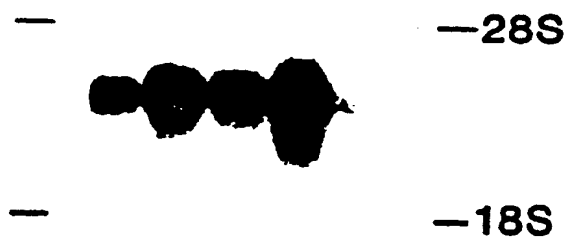


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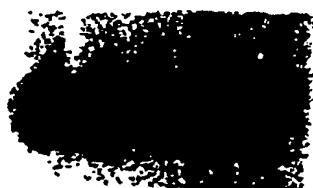
2/13

FIG. 2

PMA	-	-	+	+	+
CHX	-	+	-	+	-
Act D	-	-	-	-	+
(A)					



(B)



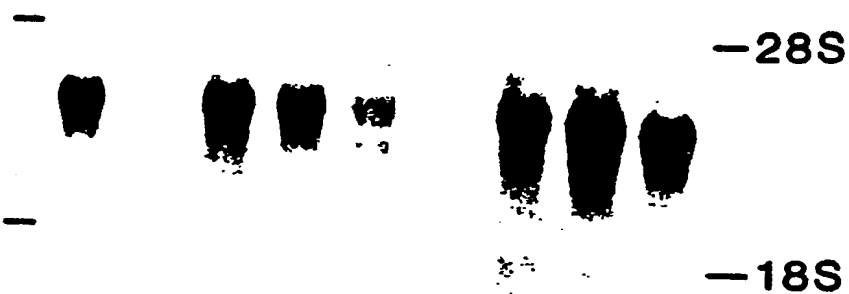
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3/13

FIG. 3

Act D	—	+	+	+	+	+	+
CHX	—	—	—	—	+	+	+
	0'	15'	30'	120'	15'	30'	120'

(A)

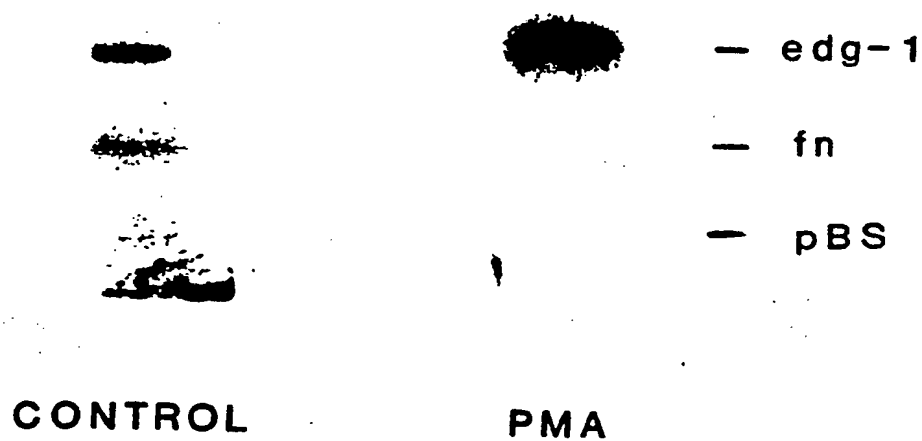


(B)

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4/13

FIG. 4



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10 TCTAAGGTC GGGGGCAGCA GCAAGATGCG AAGCGAGCCG TACAGATCCC GGGCTCTCCG AACGCAACTT 70
 80 90 100 110 120 130 140
 CGCCCTGCTT GAGCGAGGCT GCGGTTTCCG AGGCCCTCTC CAGCCAAGGA AAAGCTACAC AAAAAGCCTG 140
 150 160 170 180 190 200 210
 GATCACTCAT CGAACCACCC CTGAAGCCAG TGAAGGCTCT CTCGCCCTCGC CCTCTAGCGT TCGTCTGGAG 210
 220 230 240 250 259 268
 TAGCGCCACC CCGGCTTCCT GGGGACACAG GGTGGGCACC ATG GGG CCC ACC AGC GTC CCG
 277 286 295 304
 CTG GTC AAG GCC CAC CGC AGC TCG GTC TCT GAC TAC GTC AAC TAT GAT ATC ATC
 Leu Val Lys Ala His Arg Ser Ser Val Ser Asp Tyr Val Asn Tyr Asp Ile Ile
 331 340 349 358 367 376
 GTC CGG CAT TAC AAC TAC ACG GGA AAG CTG AAT ATC AGC GCG GAC AAG GAG AAC
 Val Arg His Tyr Asn Tyr Thr Gly Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn
 385 394 403 412 421 430
 AGC ATT AAA CTG ACC TCG GTG CTG TTC ATT CTC ATC TGC TGC TTT ATC ATC CTG
 Ser Ile Lys Leu Thr Ser Val Val Phe Ile Leu Ile Cys Cys Phe Ile Ile Leu
 439 448 457 466 475 484
 GAG AAC ATC TTT GTC TTG CTG ACC ATT TGG AAA ACC AAG AAA TTC CAC CGA CCC
 Glu Asn Ile Phe Val Leu Leu Thr Thr Ile Trp Lys Thr Lys Lys Phe His Arg Pro
 493 502 511 520 529 538
 ATG TAC TAT TTT ATT GGC AAT CTG GCC CTC TCA GAC CTG TTG GCA GGA GTA GCC
 MET Tyr Tyr Phe Ile Gly Asn Leu Ala Leu Ser Asp Leu Leu Ala Gly Val Ala

FIG. 5A

547	556	565	574	583	592
TAC ACA GCT AAC CTG CTC TTG TCT GGG GCC ACC ACC TAC AAG CTC ACT CCC GCC	Tyr Thr Ala Asn Leu Leu Leu Ser Gly Ala Thr Thr Tyr Lys Leu Thr Pro Ala				
601	610	619	628	637	646
CAG TGG TTT CTG CGG GAA GGG AGT ATG TTT GTG GCC CTG TCA GCC TCC GTG TTC	Gln Trp Phe Leu Arg Glu Gly Ser MET Phe Val Ala Leu Ser Ala Ser Val Phe				
655	664	673	682	691	700
AGT CTC CTC GCC ATC GCC ATT GAG CGC TAT ATC ACA ATG CTG AAA ATG AAA CTC	Ser Leu Leu Ala Ile Ala Ile Glu Arg Tyr Ile Thr MET Leu Lys MET Lys Leu				
709	718	727	736	745	754
CAC AAC GGG AGC AAT AAC TTC CGC CTC TTC CTG CTA ATC AGC GCC TGC TGG GTC	His Asn Gly Ser Asn Asn Phe Arg Leu Phe Leu Leu Ile Ser Ala Cys Trp Val				
763	772	781	790	799	808
ATC TCC CTC ATC CTG GGT GGC CTG CCT ATC ATG GGC TGG AAC TGC ATC AGT GCG	Ile Ser Leu Ile Leu Gly Gly Leu Pro Ile MET Gly Trp Asn Cys Ile Ser Ala				
817	826	835	844	853	862
CTG TCC AGC TGC TCC ACC GTG CTG CTG CCG CTC TAC CAC AAG CAC TAT ATC CTC TTC	Leu Ser Ser Cys Ser Thr Val Leu Leu Pro Leu Tyr Tyr His Lys His Tyr Ile Leu Phe				
871	880	889	898	907	916
TGC ACC ACG GTC TTC ACT CTG CTT CTG CTC TCC ATC ATC GTC ATT CTG TAC TGC AGA	Cys Thr Thr Val Phe Thr Leu Leu Leu Ser Ile Val Ile Leu Tyr Cys Arg				

FIG. 5B

0

925	934	943	952	961	970
ATC TAC TCC TTG GTC AGG ACT CGG AGC CGC CTG ACG TTC CGC AAG AAC ATT					
Ile Tyr Ser Leu Val Arg	0	0	0	0	0
	988	997	1006	1015	1024
TCC AAG GCC AGC AGC TCT GAG AAT GTG CCG CTG CTC AAG ACC GTA ATT ATC					
Ser Lys Ala Ser Arg Ser Glu Asn Val Ala Leu Lys	0			0	0
	1033	1042	1051	1060	1069
GTC CTG AGC GTC TTC ATC GCC TGC TGG GCA CCG CTC TTC ATC CTG CTC CTG CTG					
Val Leu Ser Val Phe Ile Ala Cys Trp Ala Pro Leu Phe Ile Leu Leu Leu Leu					
1087	1096	1105	1114	1123	1132
GAT GTG GGC TGC AAG GTG AAG ACC TGT GAC ATC CTC TTC AGA GCG GAG TAC TTC					
Asp Val Gly Cys Lys Val Lys Thr Cys Asp Ile Leu Phe Arg Ala Glu Tyr Phe					
1141	1150	1159	1168	1177	1186
CTG GTG TTA GCT GTG CTC AAC TCC GGC ACC AAC CCC ATC ATT TAC ACT CTG ACC					
Leu Val Leu Ala Val Leu Asn Ser Gly Thr Asn Pro Ile Ile Tyr Thr Leu Thr					
1195	1204	1213	1222	1231	1240
AAC AAG GAG ATG CGT CGG GCC TTC ATC CGG ATC ATG TCC TGC TGC AAG TGC CCG					
ASN Lys Glu MET Arg Arg Ala Phe Ile Arg Ile MET Ser Cys Lys Cys Pro					
1249	1258	1267	1276	1285	1294
AGC GGA GAC TCT GCT GGC AAA TTC AAG CGA CCC ATC ATC GCC GGC ATG GAA TTC					
Ser Gly Asp Ser Ala Gly Lys Phe Lys Arg Pro Ile Ile Ala Gly MET Glu Phe					

FIG. 5C

8/13

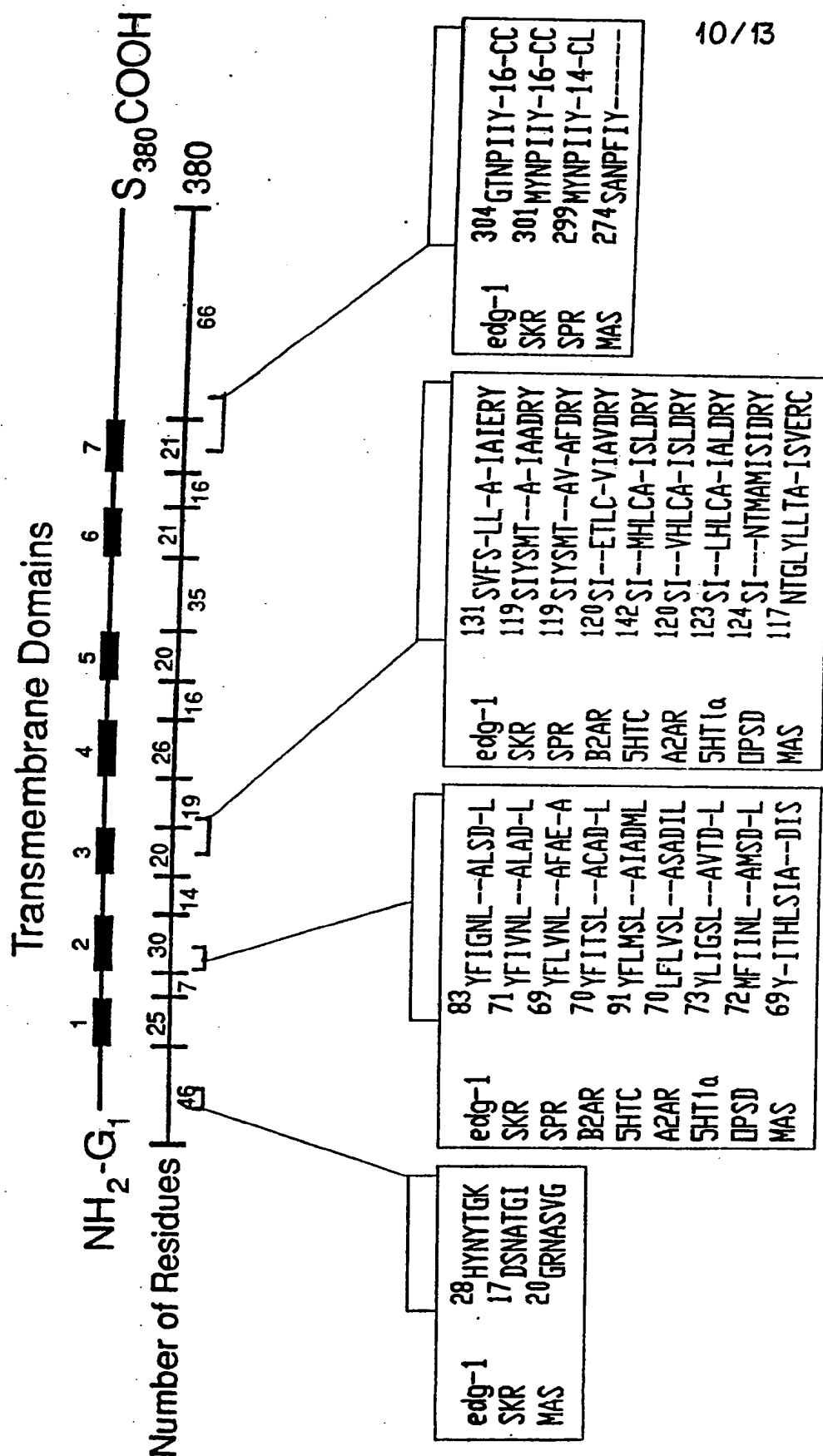
1303	1312	1321	1330	1339	1348
AGC CGC AGC AAA TCG GAC AAT TCC TCC CAC CCC CAG AAA GAC GAA GGG GAC AAC					
Ser Arg Ser Lys Ser Asp Asn Ser Ser His Pro Gln Lys Asp Glu Gly Asp Asn					
1357	1366	1375	1384	1393	1406
CCA GAG ACC ATT ATG TCT TCT GGA AAC GTC AAC TCT TCT TCC TAG AACTGGAAGC					
Pro Glu Thr Ile MET Ser Ser Gly Asn Val Asn Ser Ser Ser					
1416	1426	1436	1446	1456	1466
TGTCCACCCA CCGGAAGCGC TCTTTACTTG GTCGCTGGCC ACCCCAGTGT TTGGAAAAA ATCTCTGGGC					1476
1486	1496	1506	1516	1526	1536
TTCGACTGCT GCCAGGAGG AGCTGCTGCA AGCCAGAGGG AGGAAGGGG AGAATACGAA CAGCCTGGTG					1546
1556	1566	1576	1586	1596	1606
GTGTCGGGTG TTGGTGGGTA GAGTTAGTTC CTGTGAACAA TGCAC TGGGA AGGGTGGAGA TCAGGTCCCCG					1616
1626	1636	1646	1656	1666	1676
GCCTGGAATA TATATTCTAC CCCCCTGGAG CTTTGATTTT GCACTGAGCC AAAGGTCTAG CATTGTCAAG					1686
1696	1706	1716	1726	1736	1746
CTCCTAAAGG GTTCATTGG CCCCTCCTCA AAGACTAATG TCCCCATGTG AAAGCGTCTC TTTGTCTGGA					1756
1766	1776	1786	1796	1806	1816
GCTTTGAGGA GATGTTTCC TTCACCTTAG TTTCAAACCC AAGTGAGTGT GTGCACTTCT GCTTCTTTAG					1826
1836	1846	1856	1866	1876	1886
GGATGCCCTG TACATCCCAC ACCCCACCCT CCCTTCCCTT CATACCCCTC CTC AACGTTT TTTTACTTTA					1896
1906	1916	1926	1936	1946	1956
TACTTTAACT ACCTGAGAGT TATCAGAGCT GGGGTTGTGG AATGATCGAT CATCTATAGC AAATAGGCTA					1966
1976	1986	1996	2006	2016	2026
TGTTGAGTAC GTAGGCTGTG GGAAGATGAA GATGCTTTGG AGGTGTA AAA CAATGTCCTT CGCTGAGGCC					2036

FIG. 5D

2046	2056	2066	2076	2086	2096	2106
AAAGTTTCCA	TGTAAGCGGG	ATCCGTTTTT	TGGAATTTGG	TTGAAGTCAC	TTTGATTTCT	TTAAAAACA
2116	2126	2136	2146	2156	2166	2176
TCCTTTTCAAT	GAAATGTGTT	ACCATTTTCAT	ATCCATTGAA	GCCGAAATCT	GCATAAGGAA	GCCCACTTTA
2186	2196	2206	2216	2226	2236	2246
TCTAAATGAT	ATTAGCCAGG	ATCCTTGGTG	TCCTAGGAGA	AACAGACAAG	CAAAACAAAG	TGAAAAACCGA
2256	2266	2276	2286	2296	2306	2316
ATGGATTAAAC	TTTTGCAAAC	CAAGGGAGAT	TTCTTAGCAA	ATGAGTCTAA	CAAATATGAC	ATCCGTCCTT
2326	2336	2346	2356	2366	2376	2386
CCCACCTTTTG	TTGATGTTTA	TTTCAGAAATC	TTGTGTGATT	CATTTCAGC	AACAACATGT	TGTATTTTGT
2396	2406	2416	2426	2436	2446	2456
TGTGTTAAAA	GTAATTTTCT	TGATTTTGA	ATGTATTTGT	TTCAGGAAGA	AGTCATTTTA	TGGATTTTTC
2466	2476	2486	2496	2506	2516	2526
TAACCCGTGT	TAACTTTTCT	AGAATCCACC	CTCTTGTGCC	CTTAAGCATT	ACTTTAACTG	GTAGGGAACG
2536	2546	2556	2566	2576	2586	2596
CCAGAACTTT	TAAGTCCAGC	TATTCATTAG	ATAGTAATTG	AAGATATGTA	TAAATATTAC	AAAGAATAAA
2606	2616	2626	2636	2646	2656	2666
AATATATTAC	TGTCTCTTTA	GTATGGTTTT	CAGTGCAATT	AAACCGAGAG	ATGTCTTGTT	TTTTTAATAA
2676	2686	2696	2706	2716	2726	2736
GAATAGTATT	TAATAGGTTT	CTGACTTTTG	TGGATCATTT	TGCACATAGC	TTTATCAACT	TTTAAACATT
2746	2756	2766				
ATAAACTGA	TTTTTTTAA	GAAAAAAA	AAAAAAG			
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9/13

FIG. 5E



10/13

FIG. 6

11/13

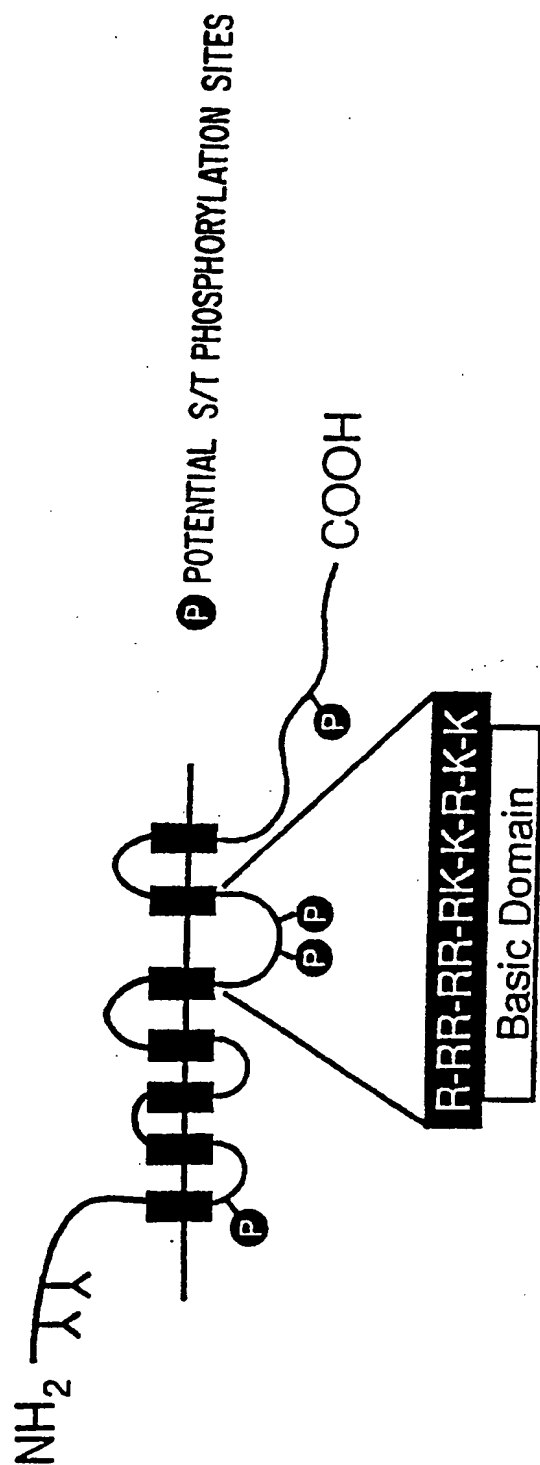


FIG. 7

12 / 13

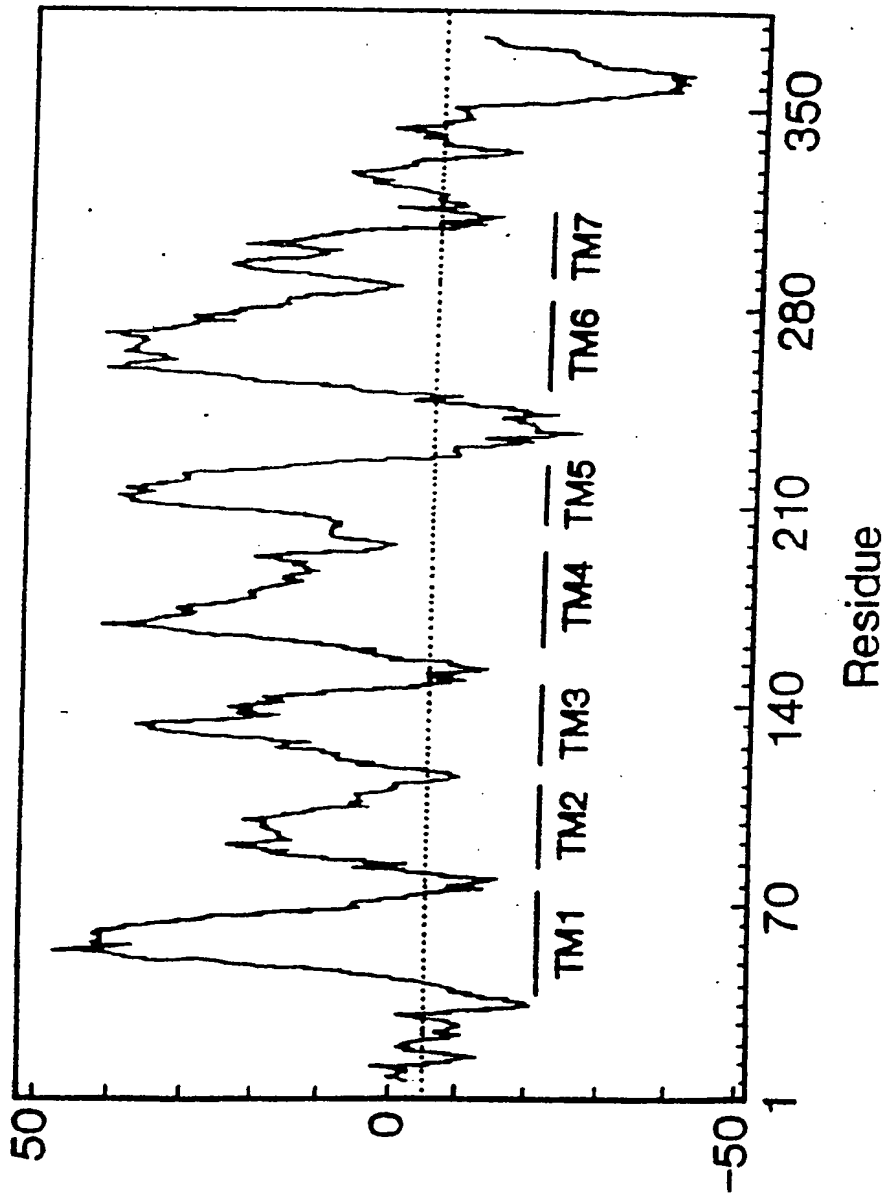


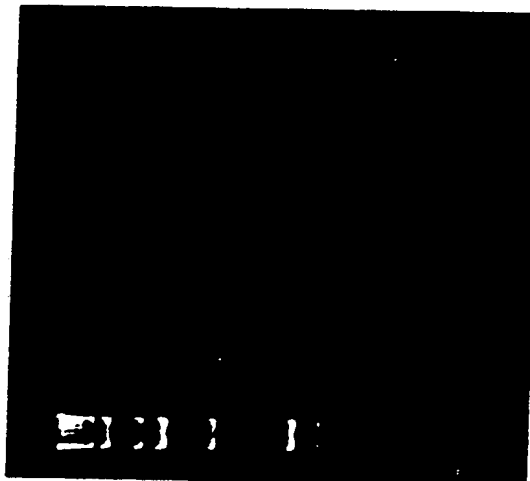
FIG. 8

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13 / 13

FIG. 9B

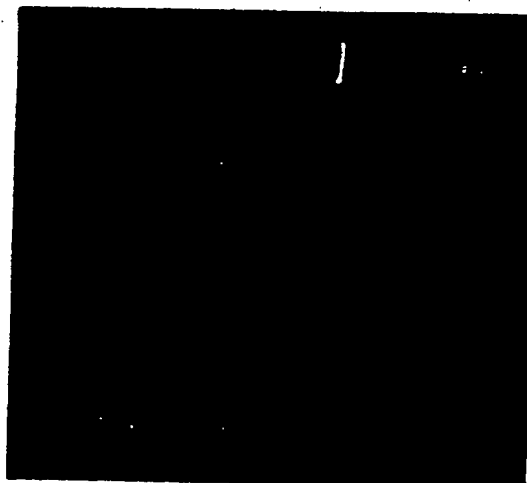
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FIG. 9A

S F A H M B E



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INTERNATIONAL SEARCH REPORT

International Application No. PCT/US91/02344

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all)

According to International Patent Classification (IPC) or to both National Classification and IPC

IPC(5): C12N 15/12; C07K 15/06, 15/14

U.S.CL.: 536/27, 530/350,395

II. FIELDS SEARCHED

Minimum Documentation Searched

Classification System	Classification Symbols
U.S.Cl.	536/27; 530/350,395.

Documentation Searched other than Minimum Documentation
to the extent that such Documents are included in the Fields Searched

APS AND DIALOG Files 357,155,WPI,72,35,5 and 399 searched
for edg type receptor proteins and sequences.

III. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of Document, ** with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
X,P	Journal of Biological Chemistry, vol. 265, No. 16, issued 05 June 1990. Hla et al., "An abundant transcript induced in differentiating human endothelial cells encodes a polypeptide with structural similarities to G-protein-coupled receptors", pages 9308-9313. See whole publication, especially the abstract, p. 9309 and 9311.	1-8
X	Science, vol. 241, issued 16 September 1988. Klein et al., "A chemoattractant receptor controls development in <u>Dictyostelium discoideum</u> ", pages 1467-1472. See whole publications, especially Figure 8 on p. 1472.	3-8
A	Science, vol. 245, issued 08 September 1989, Devreotes. " <u>Dictyostelium discoideum</u> : a model system for cell-cell interactions in development". pages 1054-1058. See whole publication.	1-8

* Special categories of cited documents: ¹⁰

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"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step

"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is compared with one or more other such documents, such combination being obvious to a person skilled in the art

"Z" document mentioned in the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search

02 July 1991

International Search Report

ISA/US

Date of Mailing of the International Search Report

26 JUL 1991

Keith C. Furman
KEITH C. FURMAN